

Genomics: GTL Contractor-Grantee Workshop VII
USDA-DOE Plant Feedstock Genomics for Bioenergy Awardee Workshop 2009
February 8-11, 2009
The Bethesda North Marriott Conference Center
North Bethesda, MD

Sunday Evening, February 8th

5:00-8:00 Registration and Poster Set Up

6:00-8:30 No-host Mixer

Monday, February 9th

7:00-8:00 Continental Breakfast

8:00-8:30 **Welcome, State of Genomics:GTL Program**
 Anna Palmisano (DOE-BER), Sharlene Weatherwax (DOE-BER),
 & Jim Fredrickson (PNNL)

8:30-9:00 **GenomicsGTL Knowledgebase Workshop Report & GTL Information Sharing Policy**
 Susan Gregurick (DOE-BER)

9:00-11:00 **Plenary Session: DOE Bioenergy Research Centers**
 Moderator: John Houghton (DOE-BER)

9:00-9:30 John Ralph, Great Lakes Bioenergy Research Center
 “Modification of cell wall structure to improve biomass processing”

9:30-10:00 Deb Mohnen, Bioenergy Sciences Center
 “Understanding Biosynthesis of Plant Cell Walls”

10:00-10:30 Break

10:30-11:00 Blake Simmons, Joint Bioenergy Institute
 "Overcoming biomass recalcitrance with ionic liquids”

11:00-12:00 **Keynote Presentation:** Antje Boetius - Max Planck Institute, Bremen
 “Methane oxidation, carbon sequestration and cellulose degradation: Lessons learned from deep sea ecosystems”

12:00-2:00 Lunch

12:30 - 2:00 Lunchtime Student Oral Presentations

Moderator: Roland Hirsch (DOE-BER)

Coordinator: Mubina Schroeder (DOE-BER)

12:30 Luke Thompson, Massachusetts Institute of Technology
 “Viruses Hijacking Cyanobacterial Carbon Metabolism”

- 12:40 Erin Heiniger, University of Washington
 “Mechanism of post-translational control of nitrogenase is revealed by analysis of constitutive hydrogen-producing mutants of *Rhodopseudomonas palustris*”
- 12:50 Ting Yang, University of Georgia
 “Functional Identification and Characterization of Sugar-1-P Kinases in Arabidopsis”
- 1:00 Mark Smith, Princeton University
 “Microalgal Biomass as Feedstock for Production of Hydrogen and Methane Fuels”
- 1:10 David Byrne, Boston University
 “Metabolic optimality and trade-offs under combinatorial genetic and nutrient modifications”
- 1:20 William Riehl, Boston University
 “Inference and integration of regulatory dynamics in metabolic network models”
- 1:30 Zhangying Hao, University of Georgia, Athens
 “GAUT12 (GALactURonosylTransferase 12): A Putative Glycosyltransferase Involved In Arabidopsis Secondary Cell Wall Biosynthesis”

2:00-5:00 **Breakout Session A: Multiscale Modeling in a Systems Biology Environment**

Moderator: Susan Gregurick & Christine Chalk

Discussion leaders: Bernhard Palsson & Jeremy Smith

To make progress in advancing our capability to predict an organism’s phenotype from the genomic sequence will require an integration of computational modeling, algorithm and software development and model-driven laboratory experimentation. To fully understand biological systems is to understand biological phenomena in their full complexity. This will require understanding of networked and responsive biological functions that are both time and context dependent and engage multi-scale processes. The goal of this session is to highlight progress made within the last year in this program and to address near and long term needs within this complex field of study.

- 2:00-2:20 Jeremy Smith, Oak Ridge National Laboratory
 “Self-Consistent Multiscale Simulation: Challenges & Prospects”
- 2:20-2:40 Mike Crowley, National Renewable Energy Laboratory
 “The Multiscale Problem of Ethanol from Biomass: From Glucose to Cell Walls, Cellulases to Cellulosomes, Methods to Supercomputer Applications”
- 2:40-3:00 Julie Mitchell, University of Wisconsin
 “Systems Biology at the Microscale: Understanding the Binding Specificity of Transcription Factors”
- 3:00-3:20 Break**
- 3:20-3:40 Bernhard Palsson, University of California, San Diego
 “Network Reconstruction for the Metabolism and Transcriptional Regulation: The Process, The Outcome, and Practical Uses”
- 3:40-4:00 Costas Maranas, Penn State University
 “Using Computations to Reconstruct, Analyze and Redesign Metabolism”
- 4:00-4:20 Adam Arkin/Paul Adams, Lawrence Berkeley National Laboratory
 “Modeling data and systems at multiple scales can drive new scientific discovery and application development”
- 4:30-5:00 Discussion Period

2:00-5:00

Breakout Session B: ELSI and Sustainability

Organizers: Dan Drell & John Houghton (DOE-BER)

Biofuels sustainability is an emerging topic that is increasing in importance as feedstock development and conversion research programs mature and as a cellulosic-based biofuels sector verges on significant expansion. Research will be critical to understand the implications of decisions that affect the sustainability in this new energy sector. The speakers will cover topics that range from economics and life cycle analysis, through carbon cycling and greenhouse gas emission implications of biofuels. An hour will be reserved for a panel discussion of integrating, GTL-relevant sustainability research.

- 2:00-2:20 Phil Robertson, Michigan State University
“Cellulosic Biofuels Sustainability: The Science Challenge”
- 2:20-2:40 Wally Tyner, Purdue University
Topic: Economic Impacts of Bioenergy
- 2:40-3:00 Madhu Khanna, University of Illinois, Urbana-Champaign
Topic: Land Use and Carbon Impacts
- 3:00-3:20 Break**
- 3:20-3:40 Stan Wullschlegel, Oak Ridge National Laboratory
Topic: Soil & Greenhouse Gas Impacts of Biomass Intensive Crops
- 3:40-4:00 Theresa Selfa, Kansas State University
“Impacts of Biofuels on Rural Communities: Preliminary Findings from Communities in Kansas and Iowa”
- 4:00-5:00 Discussion Period

2:00-5:00

Breakout Session C: Proteomics and Metabolomics: At the State of the Art

Organizer: Arthur Katz

Co- Moderators: Mary Lipton and Jonathan Sweedler

Proteomics and metabolomics have rapidly progressed from qualitatively identifying the species present to an increasingly quantitative analysis of proteins and small molecules. In that process they have morphed from testing in pure culture in the laboratory to increasingly complex environmental sampling over time. Imaging proteins and associated metals has emerged as a potential potent application as well as methods to rapidly annotate the function of proteins. This breakout session will examine a variety of new techniques and their applications in proteomics and metabolomics. It will also explore the question of how the products of these new approaches can be integrated with existing and evolving data from technologies such as fluorescent imaging and array analysis, to create a more comprehensive and potent evaluation of critical biological processes.

- 2:00-2:30 Gary Siuzdak, Scripps Institute
Topic: Imaging with Mass Spectrometry
- 2:30-3:00 Mary Lipton, Pacific Northwest National Laboratory
Topic: Metaproteomics: What can we do and what have we learned
- 3:00-3:30 Trent Northen, Lawrence Berkeley National Laboratory
Topic: Applications to cellular dynamics and protein annotation
- 3:30-3:45 Break**
- 3:45-4:15 Gavin MacBeath, Harvard University
Topic: Protein arrays and other approaches

4:15-4:45 Gordon Anderson, Pacific Northwest National Laboratory
Topic: Impacts of Bioenergy Development on Rural Communities
4:45-5:00 Discussion Period

5:00-8:00 **Poster Session**

Tuesday, February 10th

7:00-8:00 Continental Breakfast

8:00-8:30 **Joint Genome Institute Update** – Eddy Rubin, Joint Genome Institute

8:30-9:30 **Plant CyberInfrastructure** – Steve Goff, University of Arizona “The iPlant Collaborative”

9:30-10:00 Break

10:00-12:00 **Plenary Session: Plant Feedstock Genomics for Bioenergy**

Moderator: Sharlene Weatherwax

10:00-10:40 Rick Dixon, Noble Foundation
"Systematic Modification of Monolignol Pathway Gene Expression for Improved Lignocellulose Utilization"
10:40-11:20 Katrien Devos, University of Georgia
"Development of genomics resources and tools for switchgrass research"
11:20-12:00 Rex Bernardo, University of Minnesota
"Strategies for Using Molecular Markers to Simultaneously Improve Corn Grain Yield and Stover Quality for Ethanol Production"

12:00-2:00 Lunch

12:30 - 2:00 Lunchtime Student Oral Presentations

Moderator: Roland Hirsch (DOE-BER)

Coordinator: Mubina Schroeder (DOE-BER)

12:30 Zara Summers, University of Massachusetts
"Adaptive Evolution of *Geobacter sulfurreducens* under Likely Subsurface Bioremediation Conditions Revealed with Genome Resequencing"
12:40 Alireza Zomorodi, Pennsylvania State University
"Synthetic lethality analysis based on the *Escherichia coli* metabolic model"
12:50 Drew Braden, University of Wisconsin
"Catalytic Processing of Carbohydrates for the Production of Liquid Fuels"
1:00 Jin-Ying Gou, Brookhaven National Laboratory
"Characterization of pectin acetyltransferase reveals critical roles of cell wall acetyltransferase in plant growth and development"
1:10 Sridhar Ranganathan, Pennsylvania State University
"Identification of All Engineering Interventions Leading to Targeted Overproductions"
1:20 Joseph Binder, University of Wisconsin
"Simple Chemical Transformation of Lignocellulosic Biomass into Fuels and Chemicals"

2:00-5:00 **Breakout Session D: Plant Feedstock Genomics for Bioenergy**
 Moderators: Ed Kaleikau and Chavonda Jacobs-Young

This session will provide an overview of the joint USDA-DOE Plant Feedstock Genomics for Bioenergy research program leading to the improved use of biomass and plant feedstocks for the production of fuels such as ethanol or renewable chemical feedstocks. Presentations will focus on fundamental research opportunities on plants to improve biomass characteristics, biomass yield, or that will facilitate lignocellulosic degradation. Also, systems biology approaches to identify genetic indicators enabling plants to be efficiently bred or manipulated, or research that yields fundamental knowledge of the structure, function and organization of plant genomes leading to improved feedstock characterization and sustainability.

- | | |
|------------------|--|
| 2:00-2:10 | Introduction |
| 2:10-2:35 | John Vogel, USDA-ARS
“Insertional mutagenesis of <i>Brachypodium distachyon</i> ” |
| 2:35-3:00 | Pam Green, University of Delaware
“Profiling the small RNAs of <i>Brachypodium distachyon</i> ” |
| 3:00-3:20 | Break |
| 3:20-3:45 | Zhaohua Peng, Mississippi State University
“Identification of cell wall synthesis regulatory genes controlling biomass characteristics and yield in rice (<i>Oryza sativa</i>)” |
| 3:45-4:10 | Udaya Kalluri, Oak Ridge National Laboratory
“Genome-enabled discovery of carbon sequestration genes in poplar” |
| 4:10-4:35 | Eric Beers, Virginia Tech
“Towards a map of the <i>Populus</i> biomass protein-protein interaction network” |
| 4:35-5:00 | Discussion Period |

2:00-5:00 **Breakout Session E: Systems Biology Approaches to Hydrogen Production**

Moderator: Joe Graber

Co-organizers: Carrie Harwood and Josh Rabinowitz

Understanding the molecular mechanisms of biological hydrogen production requires creative new systems biology approaches. Since H₂ production pathways take a number of different forms (nitrogenase-mediated, fermentative, biophotolytic, etc.) a diverse array of model organisms must be explored. This breakout session will highlight new systems-level studies and technologies aimed at defining regulatory and metabolic networks involved in H₂ metabolism and enabling pathway engineering for enhanced H₂ production.

- | | |
|------------------|--|
| 2:00-2:20 | Carrie Harwood, University of Washington
“Transcriptomics by sequencing for hydrogen-production gene network analysis” |
| 2:20-2:40 | Josh Rabinowitz, Princeton University
“Quantitative Tools for Dissection of Hydrogen-Producing Metabolic Networks” |
| 2:40-3:00 | Himadri Pakrasi, Washington University
“Development of Cyanotheca as a New Model Organism for Biological Hydrogen Production” |
| 3:00-3:20 | Break |

3:20-3:40	Helen Kreuzer, Pacific Northwest National Laboratory “Using Hydrogen Isotopes to Assess Proton Flux During Biological Hydrogen Production”
3:40-4:00	Bob Kelly, North Carolina State University “Biohydrogenogenesis in the Thermotogales”
4:00-4:20	Robert Gunsalus, University of California, Los Angeles “Novel Hydrogen Production Systems Operative at Thermodynamic Extremes”
4:30-5:00	Panel Discussion
2:00-5:00	<p>Breakout Session F: Comparative Genomics and Annotation</p> <p>Moderator: Marvin Stodolsky</p> <p>Assignment of functionalities to genes (annotation) is rate limiting in biological research. Putative genes are today most commonly recognized within cheaply generated genome DNA sequence. Automated comparisons of putative genes with those having some prior annotation are a rational first step, relying on partial homologies between putative new genes and their priors. While a valuable first step, such annotation inherits any prior errors and should be considered a suspect resource. Additionally for microbial genomes, about a third of the putative new genes or their proteins lack homologies with priors. This breakout session reports on some new approaches to improving annotation and for functions particularly cogent to DOE missions, high throughput methods for validation.</p>
2:00-2:20	Valerie de Crecy-Lagard, University of Florida “Phylogenomics-guided validation of function for conserved unknown genes”
2:20-2:40	Andrew Bradbury, Los Alamos National Laboratory “Gene annotation by high throughput identification of binding domains”
2:40-3:00	Frank Collart, Argonne National Laboratory “Biochemical Approaches for Functional Annotation of Proteins”
3:00-3:20	Break
3:20-3:40	Andrew Tolonen, Harvard University “Annotation of the <i>Clostridium phytofermentans</i> ORFome by proteogenomic mapping <i>C. reinhardtii</i> ”
3:40-4:00	Kourosh Salehi-Ashtiani, Dana Farber Cancer Institute “Transcript verification coupled with metabolic network modeling for <i>Chlamydomonas reinhardtii</i> ”
4:00-4:20	Margie Romine, Pacific Northwest National Laboratory “Curation of the Annotation of 21 <i>Shewanella</i> Genomes: Approaches Used & Problems Revealed”
4:30-5:00	Discussion
5:00-5:30	Special Plenary Session on Metagenomics: Jo Handelsman, University of Wisconsin “Metagenomic Insights Into Environmental Sources of Antibiotic Resistance”
5:30-8:00	Poster Session

Wednesday, February 11th

- 7:00-8:00 Continental Breakfast
- 8:00-8:30 **Carbon Cycling & Biosequestration Report** Joe Graber (DOE-BER)
- 8:30-10:00 **Plenary Session: Carbon Cycling**
Moderator: Dan Drell (DOE-BER)
- 8:30 – 9:00 Alex Worden – Monterey Bay Aquarium Research Institute
“Oceans of Protists and the Carbon Cycle”
- 9:00 – 9:30 Stan Wullschleger – Oak Ridge National Laboratory
“Carbon in, Carbon out - The Fundamental Role of Plants and Microbes in Biosequestration”
- 9:30 – 10:00 Peter Thornton – Oak Ridge National Laboratory
“Plant-microbe interactions regulate climate-carbon cycle feedbacks: A new frontier for climate modeling”
- 10:00-10:30 Break
- 10:30 -11:00 Jennifer Pett-Ridge – Lawrence Livermore National Laboratory
“Stable Isotope Probes for Analysis of Nutrient Cycling”
- 11:00-11:30 Jill Banfield – University of California, Berkeley
“Rapid viral and CRISPR-based immune system co-evolution impacts carbon cycling in natural microbial communities”
- 11:30-12:00 Steve Wiley – Pacific Northwest National Laboratory
“Data Integration and Systems Biology”
- 12:00-12:30 Meeting Wrap Up & Adjournment